



SEQUENCE LISTING

<110> Lebrun, Michel
Sailland, Alain
Freyssinet, Georges
DeGryse, Eric

<120> Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase,
Gene Coding for Said Protein and Transformed Plants
Containing Said Gene

<130> 5500-13

<140> 08/945,144

<141> 1998-01-20

<150> PCT/FR96/01125

<151> 1996-07-18

<150> FRANCE 95/08979

<151> 1995-07-19

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 1713

<212> DNA

<213> Zea mays

<400> 1

aatcaatttc acacaggaaa cagctatgac catgattacg aattcgggcc cgggcgcgtg 60
atccggcgcc ggcagcggcg gcggcgggtgc aggcgggtgc cgaggagatc gtgctgcagc 120
ccatcaagga gatctccggc accgtcaagc tgccgggggc caagtcgctt tccaaccgga 180
tcctcctact cgccgccctg tccgagggga caacagtggg tgataacctg ctgaacagtg 240
aggatgtcca ctacatgctc ggggccttga ggactcttgg tctctctgtc gaagcggaca 300
aagctgccaa aagagctgta gttgttggct gtggtggaaa gttcccagtt gaggatgcta 360
aagaggaagt gcagctcttc ttggggaatg ctggaactgc aatgcggcca ttgacagcag 420
ctgttactgc tgctgggtgga aatgcaactt acgtgcttga tggagtacca agaatgaggg 480

agagacccat tggcgacttg gttgtcggat tgaagcagct tggcgcagat gttgattggt 540
 tccttggcac tgactgccca cctgttcgtg tcaatggaat cggagggcta cctgggtggca 600
 aggtcaagct gtctggctcc atcagcagtc agtacttgag tgccttgctg atggctgctc 660
 ctttggctct tggggatgtg gagattgaaa tcattgataa attaatctcc attccgtacg 720
 tcgaaatgac attgagattg atggagcgtt ttggtgtgaa agcagagcat tctgatagct 780
 gggacagatt ctacattaag ggaggtcaaa aatacaagtc ccctaaaaat gcctatgttg 840
 aagtgatgc ctcaagcgca agctatttct tggctgggtc tgcaattact ggagggactg 900
 tgactgtgga aggttgtggc accaccagtt tgcaggggtga tgtgaagttt gctgaggtac 960
 tggagatgat gggagcgaag gttacatgga ccgagactag cgtaactgtt actggcccac 1020
 cgcgggagcc atttgggagg aaacacctca aggcgattga tgtcaacatg aacaagatgc 1080
 ctgatgtcgc catgactctt gctgtgggtg ccctctttgc cgatggcccg acagccatca 1140
 gagacgtggc ttcttgaga gtaaaggaga ccgagaggat ggttgcgac cggacggagc 1200
 taaccaagct gggagcatct gttgaggaag ggccggacta ctgcatcatc acgccgccgg 1260
 agaagctgaa cgtgacggcg atcgacacgt acgacgacca caggatggcc atggccttct 1320
 cccttgccgc ctgtgccgag gtccccgtca ccatccggga ccctgggtgc acccggaaga 1380
 ccttccccga ctacttcgat gtgctgagca ctttcgtcaa gaattaataa agcgtgcat 1440
 actaccacgc agcttgattg aagtgatagg cttgtgctga ggaaatacat ttcttttgtt 1500
 ctgtttttct ctttcacggg attaagtttt gagtctgtaa cgtagttgt ttgtagcaag 1560
 tttctatttc ggatcttaag tttgtgcact gtaagccaaa tttcatttca agagtgggtc 1620
 gttggaataa taagaataat aaattacgtt tcagtgaaaa aaaaaaaaaa aaaaaaaaaa 1680
 aaaaaaaaaa aaaaaaaaaa aaccgggaa ttc 1713

<210> 2
 <211> 1340
 <212> DNA
 <213> Zea mays

<220>

<221> CDS

<222> (6)..(1337)

<400> 2

ccatg gcc gcc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc 50

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser

1

5

10

15

ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc 98

Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu

20

25

30

cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146

Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu

35

40

45

aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194

Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly

50

55

60

ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242

Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly

65

70

75

tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 290

Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu

80

85

90

95

ttc ttg ggg aat gct gga act gca atg cgg cca ttg aca gca gct gtt 338

Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val

100

105

110

act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga 386

Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg

115

120

125

atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt 434

Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu

130

135

140

ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt 482

Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg

145

150

155

gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc 530

Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly

160

165

170

175

tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg	578
Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu	
180 185 190	
gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att	626
Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile	
195 200 205	
ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa	674
Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys	
210 215 220	
gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa	722
Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln	
225 230 235	
aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc	770
Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser	
240 245 250 255	
gca agc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act	818
Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr	
260 265 270	
gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct	866
Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala	
275 280 285	
gag gta ctg gag atg atg gga gcg aag gtt aca tgg acc gag act agc	914
Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser	
290 295 300	
gta act gtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc	962
Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu	
305 310 315	
aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act	1010
Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr	
320 325 330 335	
ctt gct gtg gtt gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac	1058
Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp	
340 345 350	
gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg	1106
Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg	
355 360 365	

acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg ccg gac tac 1154
 Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr
 370 375 380

tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg 1202
 Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr
 385 390 395

tac gac gac cac agg atg gcc atg gcc ttc tcc ctt gcc gcc tgt gcc 1250
 Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala
 400 405 410 415

gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc 1298
 Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe
 420 425 430

ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa 1340
 Pro Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
 435 440

<210> 3
 <211> 444
 <212> PRT
 <213> Zea mays

<400> 3
 Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
 1 5 10 15
 Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
 20 25 30
 Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
 35 40 45
 Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
 50 55 60
 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
 65 70 75 80
 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
 85 90 95
 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
 100 105 110

Ala	Ala	Gly	Gly	Asn	Ala	Thr	Tyr	Val	Leu	Asp	Gly	Val	Pro	Arg	Met	115	120	125
Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Val	Gly	Leu	Lys	Gln	Leu	Gly	130	135	140
Ala	Asp	Val	Asp	Cys	Phe	Leu	Gly	Thr	Asp	Cys	Pro	Pro	Val	Arg	Val	145	150	155
Asn	Gly	Ile	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	165	170	175
Ile	Ser	Ser	Gln	Tyr	Leu	Ser	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	180	185	190
Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Ile	Asp	Lys	Leu	Ile	Ser	Ile	Pro	195	200	205
Tyr	Val	Glu	Met	Thr	Leu	Arg	Leu	Met	Glu	Arg	Phe	Gly	Val	Lys	Ala	210	215	220
Glu	His	Ser	Asp	Ser	Trp	Asp	Arg	Phe	Tyr	Ile	Lys	Gly	Gly	Gln	Lys	225	230	235
Tyr	Lys	Ser	Pro	Lys	Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	245	250	255
Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Gly	Thr	Val	Thr	Val	260	265	270
Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	275	280	285
Val	Leu	Glu	Met	Met	Gly	Ala	Lys	Val	Thr	Trp	Thr	Glu	Thr	Ser	Val	290	295	300
Thr	Val	Thr	Gly	Pro	Pro	Arg	Glu	Pro	Phe	Gly	Arg	Lys	His	Leu	Lys	305	310	315
Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	325	330	335
Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Ala	Ile	Arg	Asp	Val	340	345	350
Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Val	Ala	Ile	Arg	Thr	355	360	365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
 370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
 385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
 405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
 420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
 435 440

<210> 4
 <211> 1340
 <212> DNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (6)..(1337)

<400> 4
 ccatg gcc ggc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc 50
 Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser
 1 5 10 15

ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc 98
 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
 20 25 30

cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
 35 40 45

aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
 50 55 60

ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242
 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
 65 70 75

tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 290

Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu	
80 85 90 95	
ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt	338
Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val	
100 105 110	
act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga	386
Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg	
115 120 125	
atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt	434
Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu	
130 135 140	
ggg gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt	482
Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg	
145 150 155	
gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc	530
Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly	
160 165 170 175	
tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg	578
Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu	
180 185 190	
gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att	626
Ala Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile	
195 200 205	
ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aaa	674
Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys	
210 215 220	
gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa	722
Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln	
225 230 235	
aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc	770
Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser	
240 245 250 255	
gca agc tat ttc ttg gct ggt gct gca att act gga ggg act gtg act	818
Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr	
260 265 270	
gtg gaa ggt tgt ggc acc acc agt ttg cag ggt gat gtg aag ttt gct	866

Val	Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala		
			275					280					285				
gag	gta	ctg	gag	atg	atg	gga	gcg	aag	gtt	aca	tgg	acc	gag	act	agc	914	
Glu	Val	Leu	Glu	Met	Met	Gly	Ala	Lys	Val	Thr	Trp	Thr	Glu	Thr	Ser		
		290					295					300					
gta	act	gtt	act	ggc	cca	ccg	cgg	gag	cca	ttt	ggg	agg	aaa	cac	ctc	962	
Val	Thr	Val	Thr	Gly	Pro	Pro	Arg	Glu	Pro	Phe	Gly	Arg	Lys	His	Leu		
	305					310					315						
aag	gcg	att	gat	gtc	aac	atg	aac	aag	atg	cct	gat	gtc	gcc	atg	act	1010	
Lys	Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr		
320					325					330				335			
ctt	gct	gtg	gtt	gcc	ctc	ttt	gcc	gat	ggc	ccg	aca	gcc	atc	aga	gac	1058	
Leu	Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Ala	Ile	Arg	Asp		
				340					345					350			
gtg	gct	tcc	tgg	aga	gta	aag	gag	acc	gag	agg	atg	gtt	gcg	atc	cgg	1106	
Val	Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Val	Ala	Ile	Arg		
			355				360					365					
acg	gag	cta	acc	aag	ctg	gga	gca	tct	gtt	gag	gaa	ggg	ccg	gac	tac	1154	
Thr	Glu	Leu	Thr	Lys	Leu	Gly	Ala	Ser	Val	Glu	Glu	Gly	Pro	Asp	Tyr		
		370					375					380					
tgc	atc	atc	acg	ccg	ccg	gag	aag	ctg	aac	gtg	acg	gcg	atc	gac	acg	1202	
Cys	Ile	Ile	Thr	Pro	Pro	Glu	Lys	Leu	Asn	Val	Thr	Ala	Ile	Asp	Thr		
	385					390					395						
tac	gac	gac	cac	agg	atg	gcg	atg	gcc	ttc	tcc	ctt	gcc	gcc	tgt	gcc	1250	
Tyr	Asp	Asp	His	Arg	Met	Ala	Met	Ala	Phe	Ser	Leu	Ala	Ala	Cys	Ala		
400					405					410				415			
gag	gtc	ccc	gtc	acc	atc	cgg	gac	cct	ggg	tgc	acc	cgg	aag	acc	ttc	1298	
Glu	Val	Pro	Val	Thr	Ile	Arg	Asp	Pro	Gly	Cys	Thr	Arg	Lys	Thr	Phe		
				420					425					430			
ccc	gac	tac	ttc	gat	gtg	ctg	agc	act	ttc	gtc	aag	aat	taa			1340	
Pro	Asp	Tyr	Phe	Asp	Val	Leu	Ser	Thr	Phe	Val	Lys	Asn					
			435					440									

<210> 5

<211> 444

<212> PRT

<213> Zea mays

<400> 5

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
1 5 10 15

Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu
20 25 30

Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
35 40 45

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
50 55 60

Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
65 70 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
85 90 95

Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145 150 155 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175

Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
195 200 205

Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225 230 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala

	245		250		255
Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val					
	260		265		270
Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu					
	275		280		285
Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val					
	290		295		300
Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys					
	305		310		315
Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu					
		325		330	335
Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val					
	340		345		350
Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr					
	355		360		365
Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys					
	370		375		380
Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr					
	385		390		395
Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu					
		405		410	415
Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro					
	420		425		430
Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn					
	435		440		